



Molecular tracing of VHS in Denmark

Mikkelsen, Susie Sommer; Schuetze, H.; Korsholm, H.; Jensen, B. B.; Bruun, Morten Sichlau; Olesen, Niels Jørgen

Publication date:
2014

Document Version
Peer reviewed version

[Link back to DTU Orbit](#)

Citation (APA):
Mikkelsen, S. S., Schuetze, H., Korsholm, H., Jensen, B. B., Bruun, M. S., & Olesen, N. J. (2014). *Molecular tracing of VHS in Denmark*. Abstract from 18th Annual Workshop of the National Reference Laboratories for Fish Diseases, Copenhagen, Denmark.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

MOLECULAR TRACING OF VHS IN DENMARK

S. S. Mikkelsen^{*1}, H. Schuetze², H. Korsholm³, B. B. Jensen⁴, M. S. Bruun¹, N.J. Olesen¹

¹*National Veterinary Institute, Technical University of Denmark, Frederiksberg, Denmark*

²*Friedrich-Loeffler Institut, Insel Riems, Germany*

³*Danish Veterinary and Food Administration, Vejle, Denmark*

⁴*Norwegian Veterinary Institute, Oslo, Norway*

Abstract:

MOLTRAQ is a pan-European project that aims to increase knowledge on a wide array of economically important viral diseases in fish and molluscs on both the epidemiological and the genetic level. It centers on the use of spatio-temporal and phylogenetic information to create phylogeographic and scenario-simulation models to identify important factors for the spread of disease and to develop and evaluate new control strategies.

Viral haemorrhagic septicaemia Virus (VHSV) is one of the most important viral fish diseases and is widely spread all over Europe and creates significant losses every year for European fish farmers. VHSV has been endemic in Denmark since the 1950's but after an effective control and eradication programme that spanned more than 45 years the virus was finally eradicated from Denmark in 2009.

As part of MOLTRAQ more than 200 Danish isolates, including isolates from both marine and freshwater outbreaks, spanning from 1978-2003 were selected for analysis. The full-length G-gene was sequenced for all isolates and together with epidemiological information these data are being used to create phylogenetic and phylogeographic models to help infer the relationship between VHS outbreaks in Denmark and to look into the spread of the disease over a historical period as well as the effectiveness of containment and eradication programmes.

Molecular tracing shows that the numerous VHS outbreaks in marine fish farms were due to stocking these with VHS infected rainbow trout in the incubation phase and not to infection with VHSV from the marine environment. From evaluating more than 400 VHSV isolates from Denmark it appears that evolution of low virulent VHSV from marine fish species is a very rare event and is most likely related to feeding with fresh fish which is now prohibited in rainbow trout farming.

MOLTRAQ is funded under the EMIDA-ERA Net under the EU 7th Framework program.

Partners into the project are: Norwegian Veterinary Institute (NO, Coordinator), Technical University of Denmark-National Veterinary Institute (DK), Agence Nationale de Sécurité Sanitaire (FR), Friedrich-Loeffler Institut (DE), Institut Francais de Recherche pour l'Exploitation de la Mer (FR), Institut de Recherche pour le Développement (FR) and Norwegian Computing Center (NO).